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*VB*

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/155,514	11/17/98	KAINOH	M 1102-98

HM12/0615  
SCHNADER HARRISON SEGAL & LEWIS  
1600 MARKET STREET  
36TH FLOOR  
PHILADELPHIA PA 19103

EXAMINER	
SCHWADRON, R	
ART UNIT	PAPER NUMBER
1644	11

**DATE MAILED:** 06/15/00

**Please find below and/or attached an Office communication concerning this application or proceeding.**

**Commissioner of Patents and Trademarks**



UNITED STATES DEPARTMENT OF COMMERCE  
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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The communication filed on 5/3/2000 is not fully responsive to the communication mailed 4/11/2000 for the reason(s) set forth on the attached Notice to Comply With the Sequence Rules or CRF Diskette Problem Report.

Since the response appears to be bona fide, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is given **ONE (1) MONTH or THIRTY (30) DAYS** from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner Ron Schwadron, Ph.D., Art Unit 1644, whose telephone number is 703-308-4680.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

RONALD B. SCHWADRON  
PRIMARY EXAMINER  
GROUP 1800-1644

Ron Schwadron, Ph.D.  
Art Unit 1644

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216  
For CRF Submission Help, call (703) 308-4212  
For PatentIn software help, call (703) 308-6856

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

1644

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514A  
 Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

DATE: 05/18/2000  
 TIME: 07:15:09

Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: Kainoh, Mie  
 4 Tanaka, Toshiaki  
 5 <120> TITLE OF INVENTION: Chimeric proteins, their heterodimer complexes, and platelet  
 6 substitutes  
 7 <130> FILE REFERENCE: 1102-98  
 C--> 8  
 C--> 9  
 9 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00370  
 10 <151> PRIOR FILING DATE: 1997-01-29  
 11 <150> PRIOR APPLICATION NUMBER: JP 9-15118  
 12 <151> PRIOR FILING DATE: 1997-01-29  
 13 <150> PRIOR APPLICATION NUMBER: JP 9-234544  
 14 <151> PRIOR FILING DATE: 1997-08-29  
 15 <160> NUMBER OF SEQ ID: 34  
 16 <170> SOFTWARE: Microsoft Word 2000

## ERRORED SEQUENCES

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 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: 1...2958, 3316...3360, 3480...3808, 3905...4228  
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 31 -35 -30 -25  
 32 ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg 96  
 33 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Cys Leu  
 34 -20 -15 -10  
 35 ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc ggc ctg 144  
 36 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu  
 37 -5 1 5  
 38 ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg 192  
 39 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu  
 40 10 15 20 25  
 41 cac acg cac ggg ggc aac cga tgg ctc cta gtg ggt ggc ccc act gcc 240  
 42 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala  
 43 30 35 40  
 44 aac tgg ctc gcc aac gct tca gtg atc aat ccc ggg ggc att tac aga 288  
 45 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg  
 46 45 50 55  
 47 tgc acg atc gga aag aat ccc ggc cag acg tgc gaa cag ctc cag ctg 336

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
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49 60 65 70	
50 ggt agc cct aat gga gaa cct tgt gga aag act tgt ttg gaa gag aga	384
51 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg	
52 75 80 85	
55 gac aat cag tgg ttg ggg gtc aca ctt tcc aga cag cca gga gaa aat	432
56 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn	
57 90 95 100 105	
58 gga tcc atc gtc act tgt ggg cat aga tgg aaa aat ata ttt tac ata	480
59 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile	
60 110 115 120	
61 aag aat gaa aat aag ctc ccc act ggt ggt tgc tat gga gtc ccc cct	528
62 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro	
63 125 130 135	
64 gat tta cga aca gaa ctg agt aaa aga ata gct ccg tgt tat caa gat	576
65 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp	
66 140 145 150	
67 tat gtc aaa aaa ttt gga gaa aat ttt gca tca tgt caa gct gga ata	624
68 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile	
69 155 160 165	
70 tcc agt ttt tac aca aag gat tta att gtc atg ggg gcc cca gga tca	672
71 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser	
72 170 175 180 185	
73 tct tac tgg act ggc tct ctt ttt gtc tac aat ata act aca aat aaa	720
74 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys	
75 190 195 200	
76 tac aag gct ttt tta gac aaa caa aat caa gta aaa ttt gga agt tat	768
77 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr	
78 205 210 215	
79 tta gga tat tca gtc gga gct ggt cat ttt cgg agc cag cat act acc	816
80 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr	
81 220 225 230	
82 gaa gta gtc gga gga gct cct caa cat gag cag att ggt aag gca tat	864
83 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr	
84 235 240 245	
85 ata ttc agc att gat gaa aaa gaa cta aat atc tta cat gaa atg aaa	912
86 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys	
87 250 255 260 265	
88 ggt aat aag ctt gga tcc tac ttt gga gct tct gtc tgt gct gtc gac	960
89 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp	
90 270 275 280	
91 ctc aat gca gat ggc ttc tca gat ctg ctc gtg gga gca ccc atg cag	1008
92 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln	
93 285 290 295	
94 agc acc atc aga gag gaa gga aga gtc ttt gtc tac atc aac tct ggc	1056
95 Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly	
96 300 305 310	
97 tcg gga gca gta atg aat gca atg gaa aca aac ctc gtt gga agt gac	1104
98 Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514 A

DATE: 05/18/2000  
TIME: 07:15:09

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198				845		850									855		
199	ata	aaa	gct	aat	cca	cat	tgt	tta	aat	ttc	ttg	tgt	aat	ttt	ggg	aaa	2736
200	Ile	Lys	Ala	Asp	Pro	His	Cys	Leu	Asn	Phe	Leu	Cys	Asn	Phe	Gly	Lys	
201				860		865									870		
202	atg	gaa	agt	gga	aaa	gaa	gcc	agt	gtt	cat	atc	caa	ctg	gaa	ggc	cgg	2784
203	Met	Glu	Ser	Gly	Lys	Glu	Ala	Ser	Val	His	Ile	Gln	Leu	Glu	Gly	Arg	
204				875		880									885		
205	cca	tcc	att	tta	gaa	atg	gat	gag	act	tca	gca	ctc	aag	ttt	gaa	ata	2832
206	Pro	Ser	Ile	Leu	Glu	Met	Asp	Glu	Thr	Ser	Ala	Leu	Lys	Phe	Glu	Ile	
207	890				895						900				905		
208	aga	gca	aca	ggt	ttt	cca	gag	cca	aat	cca	aga	gta	att	gaa	cta	aac	2880
209	Arg	Ala	Thr	Gly	Phe	Pro	Glu	Pro	Asn	Pro	Arg	Val	Ile	Glu	Leu	Asn	
210				910		915									920		
211	aag	gat	gag	aat	gtt	gcg	cat	gtt	cta	ctg	gaa	gga	cta	cat	cat	caa	2928
212	Lys	Asp	Glu	Asn	Val	Ala	His	Val	Leu	Leu	Glu	Gly	Leu	His	His	Gln	
213				925		930									935		
214	aga	ccc	aaa	cgt	tat	tcc	acg	gat	ccc	gag	ctgcttggaa	caggctcagc					2978
215	Arg	Pro	Lys	Arg	Tyr	Phe	Thr	Asp	Pro	Glu							
216				940		945											
217	gctcctgcct	ggacgcatcc	cggctatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	ccccatgc	3038
218	gtctgcctct	tcacccggag	cctctgcctcg	ccccactcat	gtctggggag	3098											
219	ggcttttcc	caggtctcg	gcaggcacag	gttaggtgcc	cctaaacccag	ccccatgcaca	3158										
220	caaaggggca	ggtgcgtggc	tcagacatgc	caagagccat	atccggggagg	accctgc	3218										
221	tgaccta	ccacccaaa	ggccaaactc	tccactccct	cagctcg	acccatgc	3278										
222	ctccca	gatt	ccagtaactc	ccaaatttct	ctctgc	gag	ccc	aaa	tct	tgt	gac						3333
223																Glu	
224																950	
225	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	ggtaagccag	cccaaggcctc						3380
226	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro								
227				955		960											
228	gccctcc	ccgc	tcaaggcggg	acagggtccc	tagatgtgg	tgcatccagg	gacaggcc	ccccatgc	3440								
229	agccgggtgc	tgacacgtcc	acccatct	cttcctca	gca	cct	gta	ctc	ctg								3493
230																Ala	
231																965	
232	ggg	gga	ccg	tca	gtc	tcc	tcc	ccc	cca	aaa	ccc	aag	gac	acc	ctc		3541
233	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
234					970			975			980						
235	atg	atc	tcc	cg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gtg	gtg	gtg	3589
236	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
237					985			990			995						
238	cac	gaa	gac	cct	gag	gtc	aag	tcc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	3637
239	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
240	1000				1005			1010			1015						
241	gtg	cat	aat	gcc	aag	aca	aag	ccg	cg	gag	gag	cag	tac	aac	agc	acg	3685
242	Val	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr		
243					1020			1025			1030						
244	tac	cgg	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	3733
245	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	

RAW SEQUENCE LISTING  
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246	1035	1040	1045	
247	ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc			3781
248	Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
249	1050	1055	1060	
250	atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg			3828
251	Ile Glu Lys Thr Ile Ser Lys Ala Lys			
252	1065	1070		
253	aggccacat ggacagaggc cggtctggcc caccctctgc cctgagagtg accgctgtac	3888		
255	caacctctgt cctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg	3937		
256	Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu			
257	1075	1080		
258	ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc	3985		
259	Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys			
260	1085	1090	1095	
261	ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc	4033		
262	Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser			
263	1100	1105	1110	1115
264	aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gat	4081		
265	Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp			
266	1120	1125	1130	
267	tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc	4129		
268	Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser			
269	1135	1140	1145	
271	agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct	4177		
272	Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala			
273	1150	1155	1160	
274	ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa			
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	672 -25 -20 -15			
	673 tta gcg ctc agt caa ggc att tta aat tgt tgt ttg gcc tac aat gtt	96		
	674 Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val			
	675 -10 -5 1			
E-->	676 ggt ctc cca gaa gca aaa ata ttt tcc ggt cct tca agt gaa cag ttt			
	677 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe			
	678 5 10 15			
	679 ggg tat gca gtg cag cag ttt ata aat cca aaa ggc aac tgg tta ctg	192		

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TC 1500 MAIL ROOM

RAW SEQUENCE LISTING  
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Input Set : A:\1102\_98.app  
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682	gtt	ggt	tca	ccc	tgg	agt	ggc	ttt	cct	gag	aac	cga	atg	gga	gat	gtg	240	
683	Val	Gly	Ser	Pro	Trp	Ser	Gly	Phe	Pro	Glu	Asn	Arg	Met	Gly	Asp	Val		
684															50			
685	tat	aaa	tgt	cct	gtt	gac	cta	tcc	act	gcc	aca	tgt	gaa	aaa	cta	aat	288	
686	Tyr	Lys	Cys	Pro	Val	Asp	Leu	Ser	Thr	Ala	Thr	Cys	Glu	Lys	Leu	Asn		
687															65			
688	ttg	caa	act	tca	aca	agc	att	cca	aat	gtt	act	gag	atg	aaa	acc	aac	336	
689	Leu	Gln	Thr	Ser	Thr	Ser	Ile	Pro	Asn	Val	Thr	Gl	Met	Lys	Thr	Asn		
690															80			
691	atg	agc	ctc	ggc	ttg	atc	ctc	acc	agg	aac	atg	gga	act	gga	gg	ttt	384	
692	Met	Ser	Leu	Gly	Leu	Ile	Leu	Thr	Arg	Asn	Met	Gly	Thr	Gly	Gly	Phe		
693															95			
694	ctc	aca	tgt	gg	cct	ctg	tgg	gca	cag	caa	tgt	ggg	aat	cag	tat	tac	432	
695	Leu	Thr	Cys	Gly	Pro	Leu	Trp	Ala	Gln	Gln	Cys	Gly	Asn	Gln	Tyr	Tyr		
696	100					105				110						115		
697	aca	acg	gg	gt	tgt	tgt	tct	gac	atc	agt	cct	gat	ttt	cag	ctc	tca	480	
698	Thr	Thr	Gly	Val	Cys	Ser	Asp	Ile	Ser	Pro	Asp	Phe	Gln	Leu	Ser	Ala		
699																		
700	agc	ttc	tca	cct	gca	act	cag	ccc	tgc	cct	tcc	ctc	ata	gat	gtt	gt	528	
701	Ser	Phe	Ser	Pro	Ala	Thr	Gln	Pro	Cys	Pro	Ser	Leu	Ile	Asp	Val	Val		
702							135			140			145					
703	gtt	gt	tgt	gat	gaa	tca	aat	agt	att	tat	cct	tgg	gat	gca	gta	aag	576	
704	Val	Val	Cys	Asp	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys		
705							150			155			160					
706	aat	ttt	ttg	gaa	aaa	ttt	gta	caa	ggc	ctt	gat	ata	ggc	ccc	aca	aag	624	
707	Asn	Phe	Leu	Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys		
708							165			170			175					
709	aca	cag	gt	gg	tt	att	cag	tat	gcc	aat	aat	cca	aga	gtt	gt	tt	672	
710	Thr	Gln	Val	Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe		
711	180					185				190			195					
712	aac	tt	g	aa	ca	ca	tat	aaa	acc	aaa	gaa	aa	atg	att	gta	gca	aca	720
713	Asn	Leu	Asn	Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser		
714							200			205			210					
715	cag	aca	tcc	caa	tat	gg	gg	gac	ctc	aca	aa	aca	tcc	gga	gca	att	768	
716	Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile		
717							215			220			225					
718	caa	tat	gca	aga	aaa	tat	gcc	tat	tca	gca	gct	tct	gg	gg	cga	cga	816	
719	Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg		
720							230			235			240					
721	agt	gt	ac	aa	gt	at	gt	gt	act	gac	gg	gaa	tca	cat	gat	864		
722	Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp		
723							245			250			255					
724	gg	tca	at	tg	tt	aaa	gct	gt	att	gat	caa	tgc	aa	cat	gac	aa	ata	912
725	Gly	Ser	Met	Leu	Lys	Ala	Val	Ile	Asp	Gln	Cys	Asn	His	Asp	Asn	Ile		
726	260						265			270			275					
727	ctg	agg	ttt	gg	ata	gca	gtt	ctt	gg	tac	tta	aa	ac	ga	aa	cc	tt	960
728	Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu		

RAW SEQUENCE LISTING  
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729	280	285	290	
730	gat act aaa aat tta ata aaa gaa ata aaa gcg atc gct agt att cca			1008
731	Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro			
732	295	300	305	
733	aca gaa aga tac ttt ttc aat gtg tct gat gaa gca gct cta cta gaa			1056
734	Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu			
735	310	315	320	
736	aag gct ggg aca tta gga gaa caa att ttc agc att gaa ggt act gtt			1104
737	Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val			
738	325	330	335	
739	caa gga gga gac aac ttt cag atg gaa atg tca caa gtc gga ttc agt			1152
740	Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser			
741	340	345	350	355
742	gca gat tac tct tct caa aat gat att ctg atg ctg ggt gca gtc gga			1200
743	Ala Asp Tyr Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly			
744	360	365	370	
745	gct ttt ggc tgg agt ggg acc att gtc cag aag aca tct cat ggc cat			1248
746	Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His			
747	375	380	385	
748	ttg atc ttt cct aaa caa gcc ttt gac caa att ctg cag gac aga aat			1296
749	Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn			
750	390	395	400	
751	cac agt tca tat tta ggt tac tct gtc gca att tct act gga gaa			1344
752	His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu			
753	405	410	415	
754	agc act cac ttt gtt ggt gtc cct cgg gca aat tat acc ggc cag			1392
755	Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln			
756	420	425	430	435
757	ata gtc cta tat agt gtc aat gag aat ggc aat atc acg gtt att cag			1440
758	Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln			
759	440	445	450	
760	gct cac cga ggt gac cag att ggc tcc tat ttt ggt agt gtc ctg tgt			1488
761	Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys			
762	455	460	465	
763	tca gtt gat gtc gat aaa gac acc att aca gac gtc ctc ttg gta ggt			1536
764	Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly			
765	470	475	480	
766	gca cca atg tac atg agt gac cta aag aaa gag gaa gga aga gtc tac			1584
767	Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr			
768	485	490	495	
769	ctg ttt act atc aaa aag ggc att ttg ggt cag cac caa ttt ctt gaa			1632
770	Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu			
771	500	505	510	515
772	ggc ccc gag ggc att gaa aac act cga ttt ggt tca gca att gca gct			1680
773	Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala			
774	520	525	530	
775	ctt tca gac atc aac atg gat ggc ttt aat gat gtc att gtt ggt tca			1728
776	Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser			
777	535	540	545	

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778 cca cta gaa aat cag aat tct gga gct gta tac att tac aat ggt cat	1776
779 Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Asn Gly His	
780 550 555 560	
781 cag ggc act atc cgc aca aag tat tcc cag aaa atc ttg gga tcc gat	1824
782 Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp	
783 565 570 575	
784 gga gcc ttt agg agc cat ctc cag tac ttt ggg agg tcc ttg gat ggc	1872
785 Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly	
786 580 585 590 595	
787 tat gga gat tta aat ggg gat tcc atc acc gat gtg tct att ggt gcc	1920
788 Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala	
789 600 605 610	
790 ttt gga caa gtg gtt caa ctc tgg tca caa agt att gct gat gta gct	1968
791 Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala	
792 615 620 625	
793 ata gaa gct tca ttc aca cca gaa aaa atc act ttg gtc aac aag aat	2016
794 Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn	
795 630 635 640	
796 gct cag ata att ctc aaa ctc tgc ttc agt gca aag ttc aga cct act	2064
797 Aia Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr	
798 645 650 655	
799 aag caa aac aat caa gtg gcc att gta tat aac atc aca ctt gat gca	2112
800 Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala	
801 660 665 670 675	
802 gat gga ttt tca tcc aga gta acc tcc agg ggg tta ttt aaa gaa aac	2160
803 Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn	
804 680 685 690	
805 aat gaa agg tgc ctg cag aag aat atg gta gta aat caa gca cag agt	2208
806 Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser	
807 695 700 705	
808 tgc ccc gag cac atc att tat ata cag gag ccc tct gat gtt gtc aac	2256
809 Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn	
810 710 715 720	
811 tct ttg gat ttg cgt gtg gac atc agt ctg gaa aac cct ggc act agc	2304
812 Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser	
813 725 730 735	
814 cct gcc ctt gaa gcc tat tct gag act gcc aag gtc ttc agt att cct	2352
815 Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro	
816 740 745 750 755	
817 ttc cac aaa gac tgt ggt gag gat gga ctt tgc att tct gat cta gtc	2400
818 Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val	
819 760 765 770	
820 cta gat gtc cga caa ata cca gct gct caa gaa caa ccc ttt att gtc	2448
821 Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val	
822 775 780 785	
823 agc aac caa aac aaa agg tta aca ttt tca gta aca ctg aaa aat aaa	2496
824 Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys	
825 790 795 800	
826 agg gaa agt gca tac aac act gga att gtt gtt ttt tca gaa aac	2544

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827 Arg Glu Ser Ala Tyr Asn Thr Gly Ile Val Val Asp Phe Ser Glu Asn			
828 805	810	815	
829 ttg ttt ttt gca tca ttc tcc cta ccg gtt gat ggg aca gaa gta aca		2592	
830 Leu Phe Phe Ala Ser Phe Ser Leu Pro Val Asp Gly Thr Glu Val Thr			
831 820	825	830	835
832 tgc cag gtg gct gca tct cag aag tct gtt gcc tgc gat gta ggc tac		2640	
833 Cys Gln Val Ala Ala Ser Gln Lys Ser Val Ala Cys Asp Val Gly Tyr			
834 840	845	850	850
835 cct gct tta aag aga gaa caa cag gtg act ttt act att aac ttt gac		2688	
836 Pro Ala Leu Lys Arg Glu Gln Gln Val Thr Phe Thr Ile Asn Phe Asp			
837 855	860	865	865
838 ttc aat ctt caa aac ctt cag aat cag gcg tct ctc agt ttc caa gcc		2736	
839 Phe Asn Leu Gln Asn Leu Gln Asn Gln Ala Ser Leu Ser Phe Gln Ala			
840 870	875	880	880
841 tta agt gaa agc caa gaa aac aag gct gat aat ttg gtc aac ctc		2784	
842 Leu Ser Glu Ser Gln Glu Glu Asn Lys Ala Asp Asn Leu Val Asn Leu			
843 885	890	895	895
844 aaa att cct ctc ctg tat gat gct gaa att cac tta aca aga tct acc		2832	
845 Lys Ile Pro Leu Leu Tyr Asp Ala Glu Ile His Leu Thr Arg Ser Thr			
846 900	905	910	915
847 aac ata aat ttt tat gaa atc tct tcg gat ggg aat gtt cct tca atc		2880	
848 Asn Ile Asn Phe Tyr Glu Ile Ser Ser Asp Gly Asn Val Pro Ser Ile			
849 920	925	930	930
850 gtg cac agt ttt gaa gat gtt ggt cca aaa ttc atc ttc tcc ctg aag		2928	
851 Val His Ser Phe Glu Asp Val Gly Pro Lys Phe Ile Phe Ser Leu Lys			
852 935	940	945	945
853 gta aca aca gga agt gtt cca gta agc atg gca act gta atc atc cac		2976	
854 Val Thr Thr Gly Ser Val Pro Val Ser Met Ala Thr Val Ile Ile His			
855 950	955	960	960
856 atc cct cag tat acc aaa gaa aag aac cca ctg atg tac cta act ggg		3024	
857 Ile Pro Gln Tyr Thr Lys Glu Lys Asn Pro Leu Met Tyr Leu Thr Gly			
858 965	970	975	975
859 gtg caa aca gac aag gct ggt gac atc agt tgt aat gca gat atc aat		3072	
860 Val Gln Thr Asp Lys Ala Gly Asp Ile Ser Cys Asn Ala Asp Ile Asn			
861 980	985	990	995
862 cca ctg aaa ata gga caa aca tct tct gta tct ttc aaa agt gaa		3120	
863 Pro Leu Lys Ile Gly Gln Thr Ser Ser Val Ser Val Phe Lys Ser Glu			
864 1000	1005	1010	1010
865 aat ttc agg cac acc aaa gaa ttg aac tgc aga act gct tcc tgt agt		3168	
866 Asn Phe Arg His Thr Lys Glu Leu Asn Cys Arg Thr Ala Ser Cys Ser			
867 1015	1020	1025	1025
868 aat gtt acc tgc tgg ttg aaa gac gtt cac atg aaa gga gaa tac ttt		3216	
869 Asn Val Thr Cys Trp Leu Lys Asp Val His Met Lys Gly Glu Tyr Phe			
870 1030	1035	1040	1040
871 gtt aat gtg act acc aga att tgg aac ggg act ttc gca tca tca acg		3264	
872 Val Asn Val Thr Thr Arg Ile Trp Asn Gly Thr Phe Ala Ser Ser Thr			
873 1045	1050	1055	1055
874 ttc cag aca gta cag cta acg gca gct gca gaa atc aac acc tat aac		3312	
875 Phe Gln Thr Val Gln Leu Thr Ala Ala Glu Ile Asn Thr Tyr Asn			

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876	1060	1065	1070	1075				
877	cct gag ata tat	gtg att gaa gat aac	act gtt acg att	ccc ctg atg	3360			
878	Pro Glu Ile Tyr	Val Ile Glu Asp	Asn Thr Val Thr	Ile Pro Leu Met				
879	1080	1085	1090					
880	ata atg aaa cct	gat gag aaa gcc	gaa gta cca aca	gat ccc gag	3405			
881	Ile Met Lys Pro	Asp Glu Lys Ala	Glu Val Pro	Thr Asp Pro Glu				
882	1095	1100	1105					
883	ctgcttggaa	caggctcagc	gctctgcct	ggacgcatcc	cggctatgca	gccccagtc	3465	
884	agggcagcaa	ggcaggcccc	gtctgcctct	tcacccggag	cctctgccc	ccccactcat	3525	
885	gctcaggag	agggtctct	ggctttttcc	caggctctgg	gcaggcacag	gttaggtcc	3585	
886	cctaaccagg	gccctgcaca	caaaggggca	ggtgctggc	tcagacctgc	caagagccat	3645	
887	atccggagg	accctgcccc	tgacctaagc	ccacccaaaa	ggccaaactc	tccactccct	3705	
888	cagctcggac	accttctctc	ctcccaagatt	ccagtaactc	ccaatcttct	ctctgca	3762	
889	gag ccc aaa tct	tgt gac aaa	act cac aca	tgc cca ccg	tgc cca		3807	
890	Glu Pro Lys Ser	Cys Asp Lys	Thr His	Thr Cys Pro	Pro Pro Cys Pro			
891	1110	1115	1120					
892	ggtaagccag	cccaggccctc	gccctccagc	tcaaggcggg	acaggtgccc	tagatgacc	3867	
893	tgcatccagg	gacaggcccc	agccgggtgc	tgacacgtcc	acctccatct	cttcctca	3925	
894	gca cct gaa	ctc ctg ggg	ggg ccc tca	gtc ttc ctc	ttc ccc cca	aaa	3973	
895	Ala Pro Glu	Leu Leu Gly	Gly Pro Ser	Val Phe Leu	Phe Pro Pro Lys			
896	1125	1130	1135					
897	ccc aag gac	acc ctc atg	atc tcc cgg	acc cct gag	gtc aca tgc	gtg 4021		
898	Pro Lys Asp	Thr Leu Met	Ile Ser Arg	Thr Pro Glu	Val Thr Cys Val			
899	1140	1145	1150					
900	gtg gtg gac	gtg agc cac	gaa gac cct	gag gtc aag ttc	aac tgg tac		4069	
901	Val Val Asp	Val Ser His	Glu Asp Pro	Glu Val Lys	Phe Asn Trp Tyr			
902	1155	1160	1165					
904	gtg gac ggc	gtg gag gtg	cat aat gcc	aag aca aag	ccg cgg gag	gag 4117		
905	Val Asp Gly	Val Glu Val	His Asn Ala	Lys Thr Lys	Pro Arg Glu Glu			
906	1170	1175	1180	1185				
907	cag tac aac	agc acg tac	cgg gtg	gtc agc gtc	ctc acc gtc	ctg cac	4165	
908	Gln Tyr Asn Ser	Thr Tyr Arg	Val Val Ser	Val Leu Thr	Val Leu His			
909	1190	1195	1200					
910	cag gac tgg	ctg aat ggc	aag gag tac	aag tgc aag	gtc tcc aac	aaa 4213		
911	Gln Asp Trp	Leu Asn Gly	Lys Glu Tyr	Lys Cys Lys	Val Ser Asn Lys			
912	1205	1210	1215					
913	gcc ctc cca	gcc ccc atc	gag aaa acc	atc tcc	aaa gcc	aaa 4255		
914	Ala Leu Pro	Ala Pro Ile	Glu Lys Thr	Ile Ser Lys	Ala Lys			
915	1220	1225	1230					
916	ggtggaccc	gtgggggtcg	aggccacat	ggacagaggc	cggctcgccc	caccctctgc	4315	
917	cctgagatg	accgcgtac	caacctctgt	cctaca	ggg cag	ccc cga gaa cca	4369	
918					Gly	Gln Pro Arg Glu Pro		
919				1235				
920	cag gtg tac	acc ctg ccc	cca tcc cgg	gat gag ctg	acc aag aac	cag 4417		
921	Gln Val	Tyr Thr Leu	Pro Pro Ser	Arg Asp Glu	Leu Thr Lys	Asn Gln		
922	1240	1245	1250					
923	gtc agc ctg	acc tgc ctg	gtc aaa ggc	tcc tat ccc	agc gac atc	gcc 4465		
924	Val Ser Leu	Thr Cys Leu	Val Lys Gly	Phe Tyr Pro Ser	Asp Ile Ala			
925	1255	1260	1265					

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926 gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg 4513  
927 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
928 1270 1275 1280 1285  
929 cct ccc gtg ctg gat tcc gac ggc tcc ttc ttc ctc tac agc aag ctc 4561  
930 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
931 1290 1295 1300  
932 acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc 4609  
933 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
934 1305 1310 1315  
935 gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc 4657  
936 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
937 1320 1325 1330  
938 ctg tct ccg ggt aaa tga 4675  
939 Leu Ser Pro Gly Lys  
940 1335  
1077 <210> SEQ ID NO: 32  
1078 <211> LENGTH: 1179  
1079 <212> TYPE: PRT  
1080 <213> ORGANISM: Homo sapien  
1082 <400> SEQUENCE: 32  
1083 Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro  
1084 -35 -30 -25  
1086 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Cys Leu  
1087 -20 -15 -10  
1089 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu  
1090 -5 1 5  
1092 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu  
1093 10 15 20 25  
1095 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala  
1096 30 35 40  
1098 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg  
1099 45 50 55  
1101 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu  
1102 60 65 70  
1104 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg  
1105 75 80 85  
1107 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn  
1108 90 95 100 105  
1110 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile  
1111 110 115 120  
1113 Lys Asn Glu Asn Lys Leu Pro Thr Gly Cys Tyr Gly Val Pro Pro  
1114 125 130 135  
1116 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp  
1117 140 145 150  
1119 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile  
1120 155 160 165  
1122 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser  
1123 170 175 180 185  
1125 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys

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(2117 response)

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1126	190	195	200
1128	Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Val Lys Phe Gly Ser Tyr		
1129	205	210	215
1131	Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr		
1132	220	225	230
1135	Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr		
1136	235	240	245
1138	Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys		
1139	250	255	260
1141	Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp		
1142	270	275	280
1144	Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln		
1145	285	290	295
1147	Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly		
1148	300	305	310
1150	Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp		
1151	315	320	325
1153	Lys Tyr Ala Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile		
1154	330	335	340
1156	Asp Asn Asp Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp		
1157	350	355	360
1159	Asp Leu Gln Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile		
1160	365	370	375
1162	Ser Ser Thr Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser		
1163	380	385	390
1165	Leu Ser Met Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn		
1166	395	400	405
1168	Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala		
1169	410	415	420
1171	425		
1172	Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser		
1174	430	435	440
1175	His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly		
1177	445	450	455
1178	Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly		
1180	460	465	470
1181	Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp		
1183	475	480	485
1184	Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn		
1186	490	495	500
1186	505		
1187	Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu		
1189	510	515	520
1190	Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp		
1192	525	530	535
1193	Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His		
1195	540	545	550
1196	Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile		
1198	555	560	565
1199	Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe		
	570	575	580
			585

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1201 Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser  
 1202 590 595 600  
 1204 Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala  
 1205 605 610 615  
 1207 Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala  
 1208 620 625 630  
 1210 Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly  
 1211 635 640 645  
 1213 Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Lys Gln Ile Asn Cys  
 1214 650 655 660 665  
 1216 Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly  
 1217 670 675 680  
 1219 Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu  
 1220 685 690 695  
 1222 Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val  
 1223 700 705 710  
 1225 His Ala Thr Cys Glu Asn Glu Glu Met Asp Asn Leu Lys His Ser  
 1226 715 720 725  
 1228 Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val  
 1229 730 735 740 745  
 1231 His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu  
 1232 750 755 760  
 1234 Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His  
 1235 765 770 775  
 1237 Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile  
 1238 780 785 790  
 1240 Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile  
 1241 795 800 805  
 1243 Leu Asp Val Gln Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln  
 1244 810 815 820 825  
 1246 Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys  
 1247 830 835 840  
 1249 Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys  
 1250 845 850 855  
 1252 Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys  
 1253 860 865 870  
 1255 Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg  
 1256 875 880 885  
 1258 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile  
 1259 890 895 900 905  
 1261 Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn  
 1262 910 915 920  
 1264 Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln  
 1265 925 930 935  
 1267 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu Glu Pro Lys Ser Cys Asp  
 1268 940 945 950  
 1270 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 1271 955 960 965  
 1273 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
 TIME: 07:15:09

Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\1155514.raw

1274 970 975 980 985  
 1276 Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu  
 1277 990 995 1000  
 1279 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His  
 1280 1005 1010 1015  
 1282 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg  
 1283 1020 1025 1030  
 1285 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys  
 1286 1035 1040 1045  
 1288 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu  
 1289 1050 1055 1060 1065  
 1291 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr  
 1292 1070 1075 1080  
 1294 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu  
 1295 1085 1090 1095  
 1297 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp  
 1298 1100 1105 1110  
 1300 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val  
 1301 1115 1120 1125  
 1303 Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val Asp  
 1304 1130 1135 1140 1145  
 1306 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His  
 1307 1150 1155 1160  
 1309 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 1310 1165 1170 1175

E--> 1312 Gly Lys

1315 <210> SEQ ID NO: 33  
 1316 <211> LENGTH: 943 (963/p.18)  
 1317 <212> TYPE: PRT  
 1318 <213> ORGANISM: Homo sapien  
 1320 <400> SEQUENCE: 33  
 1323 Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys  
 1324 -20 -15 -10 -5  
 1326 Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala  
 1327 1 5 10  
 1329 Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys  
 1330 15 20 25  
 1332 Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys  
 1333 30 35 40  
 1335 Asp Asp Leu Glu Ala Leu Lys Lys Gly Cys Pro Pro Asp Asp Ile  
 1336 45 50 55 60  
 1338 Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr  
 1339 65 70 75  
 1341 Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His  
 1342 - 80 85 90  
 1344 Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro  
 1345 95 100 105  
 1347 Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp  
 1348 110 115 120

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000  
TIME: 07:15:09

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

1351 Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu  
1352 125 130 135 140  
1354 Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile  
1355 145 150 155  
1357 Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val  
1358 160 165 170  
1360 Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr  
1361 175 180 185  
1363 Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser  
1364 190 195 200  
1366 Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg  
1367 205 210 215 220  
1369 Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met  
1370 225 230 235  
1372 Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg  
1373 240 245 250  
1375 Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly  
1376 255 260 265  
1378 Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu  
1379 270 275 280  
1381 Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala  
1382 285 290 295 300  
1384 His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala  
1385 305 310 315  
1387 Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile  
1388 320 325 330  
1390 Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile  
1391 335 340 345  
1393 Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu  
1394 350 355 360  
1396 Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr  
1397 365 370 375 380  
1399 Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser  
1400 385 390 395  
1402 Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser  
1403 400 405 410  
1405 Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu  
1406 415 420 425  
1408 Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys  
1409 430 435 440  
1411 Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly  
1412 445 450 455 460  
1414 Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val  
1415 465 470 475  
1417 Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met  
1418 480 485 490  
1420 Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn  
1421 495 500 505  
1423 Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
 TIME: 07:15:09

Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

1424	510	515	520
1426	Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys		
1427	525	530	535
1429	Asp Arg Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys		540
1430	545	550	555
1432	Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys		
1433	560	565	570
1435	Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn		
1436	575	580	585
1438	Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys		
1439	590	595	600
1441	Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys		
1442	605	610	615
1444	Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu		620
1445	625	630	635
1447	Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys		
1448	640	645	650
1450	Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val		
1451	655	660	665
1453	Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr		
1454	670	675	680
1456	Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn		
1457	685	690	695
1459	700		
1460	Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu Glu Pro Lys Ser Cys		
1462	705	710	715
1463	Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly		
1465	720	725	730
1466	Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		
1466	735	740	745
1468	Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His		
1469	750	755	760
1471	Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val		
1472	765	770	775
1474	780		
1474	His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr		
1475	785	790	795
1477	Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		
1478	800	805	810
1480	Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile		
1481	815	820	825
1483	Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val		
1484	830	835	840
1486	Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser		
1487	845	850	855
1489	860		
1489	Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		
1490	865	870	875
1492	Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro		
1493	880	885	890
1495	Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val		
1496	895	900	905

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102\_98.app

Output Set: N:\CRF3\05182000\I155514.raw

1498 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 1499 910 915 920  
 1501 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 1502 925 930 935 940

E--&gt; 1504 Pro Gly Lys

1506 <210> SEQ ID NO: 34  
 1507 <211> LENGTH: 1338  
 1508 <212> TYPE: PRT

1367 (p. 21)

1509 &lt;213&gt; ORGANISM: Homo sapien

W--&gt; 1510 &lt;300&gt; PUBLICATION INFORMATION:

1512 &lt;400&gt; SEQUENCE: 34

1513 Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val  
 1514 -25 -20 -15  
 1516 Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val  
 1517 -10 -5 1  
 1519 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe  
 1520 5 10 15  
 1522 Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu  
 1523 20 25 30 35  
 1525 Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val  
 1526 40 45 50  
 1528 Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn  
 1529 55 60 65  
 1531 Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn  
 1532 70 75 80  
 1534 Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Phe  
 1535 85 90 95  
 1537 Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr  
 1538 100 105 110 115  
 1540 Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala  
 1541 120 125 130  
 1543 Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val  
 1544 135 140 145  
 1546 Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys  
 1547 150 155 160  
 1549 Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys  
 1550 165 170 175  
 1552 Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe  
 1553 180 185 190 195  
 1555 Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser  
 1556 200 205 210  
 1558 Gln Thr Ser Gln Tyr Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile  
 1559 215 220 225  
 1561 Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg  
 1562 230 235 240  
 1564 Ser Ala Thr Lys Val Met Val Val Thr Asp Gly Glu Ser His Asp  
 1565 245 250 255  
 1567 Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile  
 1568 260 265 270 275

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514

DATE: 05/18/2000

TIME: 07:15:09

Input Set : A:\1102\_98.app

Output Set: N:\CRF3\05182000\I155514.raw

1570 Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu  
 1571 280 285 290  
 1573 Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro  
 1574 295 300 305  
 1576 Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu  
 1577 310 315 320  
 1579 Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val  
 1580 325 330 335  
 1582 Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser  
 1583 340 345 350 355  
 1585 Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly  
 1586 360 365 370  
 1588 Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His  
 1589 375 380 385  
 1591 Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn  
 1592 390 395 400  
 1594 His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu  
 1595 405 410 415  
 1597 Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln  
 1598 420 425 430 435  
 1600 Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln  
 1601 440 445 450  
 1603 Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys  
 1604 455 460 465  
 1606 Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly  
 1607 470 475 480  
 1609 Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Gly Arg Val Tyr  
 1610 485 490 495  
 1612 Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu  
 1613 500 505 510 515  
 1615 Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala  
 1616 520 525 530  
 1618 Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser  
 1619 535 540 545  
 1621 Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His  
 1622 550 555 560  
 1624 Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp  
 1625 565 570 575  
 1627 Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly  
 1628 580 585 590 595  
 1630 Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala  
 1631 600 605 610  
 1633 Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala  
 1634 615 620 625  
 1636 Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn  
 1637 630 635 640  
 1639 Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr  
 1640 645 650 655  
 1642 Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
 TIME: 07:15:09

Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

1643	660	665	670	675													
1645	Asp	Gly	Phe	Ser	Ser	Arg	Val	Thr	Ser	Arg	Gly	Leu	Phe	Lys	Glu	Asn	
1646																	690
1648	Asn	Glu	Arg	Cys	Leu	Gln	Lys	Asn	Met	Val	Val	Asn	Gln	Ala	Gln	Ser	
1649																	705
1651	Cys	Pro	Glu	His	Ile	Ile	Tyr	Ile	Gln	Glu	Pro	Ser	Asp	Val	Val	Asn	
1652																	720
1654	Ser	Leu	Asp	Leu	Arg	Val	Asp	Ile	Ser	Leu	Glu	Asn	Pro	Gly	Thr	Ser	
1655																	735
1657	Pro	Ala	Leu	Glu	Ala	Tyr	Ser	Glu	Thr	Ala	Lys	Val	Phe	Ser	Ile	Pro	
1658																	755
1660	Phe	His	Lys	Asp	Cys	Gly	Glu	Asp	Gly	Leu	Cys	Ile	Ser	Asp	Leu	Val	
1661																	770
1663	Leu	Asp	Val	Arg	Gln	Ile	Pro	Ala	Ala	Gln	Glu	Gln	Pro	Phe	Ile	Val	
1664																	785
1666	Ser	Asn	Gln	Asn	Lys	Arg	Leu	Thr	Phe	Ser	Val	Thr	Leu	Lys	Asn	Lys	
1667																	800
1669	Arg	Glu	Ser	Ala	Tyr	Asn	Thr	Gly	Ile	Val	Val	Asp	Phe	Ser	Glu	Asn	
1670																	815
1672	Leu	Phe	Phe	Ala	Ser	Phe	Ser	Leu	Pro	Val	Asp	Gly	Thr	Glu	Val	Thr	
1673																	835
1675	Cys	Gln	Val	Ala	Ala	Ser	Gln	Lys	Ser	Val	Ala	Cys	Asp	Val	Gly	Tyr	
1676																	850
1678	Pro	Ala	Leu	Lys	Arg	Glu	Gln	Gln	Val	Thr	Phe	Thr	Ile	Asn	Phe	Asp	
1679																	865
1681	Phe	Asn	Leu	Gln	Asn	Leu	Gln	Asn	Gln	Ala	Ser	Leu	Ser	Phe	Gln	Ala	
1682																	880
1684	Leu	Ser	Glu	Ser	Gln	Glu	Glu	Asn	Lys	Ala	Asp	Asn	Leu	Val	Asn	Leu	
1685																	895
1687	Lys	Ile	Pro	Leu	Leu	Tyr	Asp	Ala	Glu	Ile	His	Leu	Thr	Arg	Ser	Thr	
1688																	915
1690	Asn	Ile	Asn	Phe	Tyr	Glu	Ile	Ser	Ser	Asp	Gly	Asn	Val	Pro	Ser	Ile	
1691																	930
1693	Val	His	Ser	Phe	Glu	Asp	Val	Gly	Pro	Lys	Phe	Ile	Phe	Ser	Leu	Lys	
1694																	945
1696	Val	Thr	Thr	Gly	Ser	Val	Pro	Val	Ser	Met	Ala	Thr	Val	Ile	Ile	His	
1697																	960
1699	Ile	Pro	Gln	Tyr	Thr	Lys	Glu	Lys	Asn	Pro	Leu	Met	Tyr	Leu	Thr	Gly	
1700																	975
1702	Val	Gln	Thr	Asp	Lys	Ala	Gly	Asp	Ile	Ser	Cys	Asn	Ala	Asp	Ile	Asn	
1703																	995
1705	Pro	Leu	Lys	Ile	Gly	Gln	Thr	Ser	Ser	Ser	Val	Ser	Phe	Lys	Ser	Glu	
1706																	1010
1708	Asn	Phe	Arg	His	Thr	Lys	Glu	Leu	Asn	Cys	Arg	Thr	Ala	Ser	Cys	Ser	
1709																	1025
1711	Asn	Val	Thr	Cys	Trp	Leu	Lys	Asp	Val	His	Met	Lys	Gly	Glu	Tyr	Phe	
1712																	1040
1714	Val	Asn	Val	Thr	Thr	Arg	Ile	Trp	Asn	Gly	Thr	Phe	Ala	Ser	Ser	Thr	
1715																	1055

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514 A DATE: 05/18/2000  
 TIME: 07:15:09

Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

1717 Phe Gln Thr Val Gln Leu Thr Ala Ala Ala Glu Ile Asn Thr Tyr Asn  
 1718 1060 1065 1070 1075  
 1720 Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met  
 1721 1080 1085 1090  
 1723 Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu Glu  
 1724 1095 1100 1105  
 1726 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
 1727 1110 1115 1120  
 1729 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 1730 1125 1130 1135  
 1732 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 1733 1140 1145 1150 1155  
 1735 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 1736 1160 1165 1170  
 1738 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
 1739 1175 1180 1185  
 1741 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
 1742 1190 1195 1200  
 1744 Trp Leu Asn Gly Lys Glu Tyr Lys, Cys Lys Val Ser Asn Lys Ala Leu  
 1745 1205 1210 1215  
 1747 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
 1748 1220 1225 1230 1235  
 1750 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys  
 1751 1240 1245 1250  
 1753 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 1754 1255 1260 1265  
 1756 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 1757 1270 1275 1280  
 1759 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 1760 1285 1290 1295  
 1762 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 1763 1300 1305 1310 1315  
 1765 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 1766 1320 1325 1330  
 1768 Leu Ser Leu Ser Pro Gly Lys  
 E--> 1769 1335

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
TIME: 07:15:10

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier  
L:7 M:283 W: Missing Blank Line separator, <130> field identifier  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:283 W: Missing Blank Line separator, <160> field identifier  
L:22 M:283 W: Missing Blank Line separator, <220> field identifier  
L:25 M:283 W: Missing Blank Line separator, <300> field identifier  
L:187 M:254 E: (42) Number of Bases conflicts Running Total, LENGTH:Input:2588 Counted:2544  
L:284 M:283 W: Missing Blank Line separator, <220> field identifier  
L:287 M:283 W: Missing Blank Line separator, <300> field identifier  
L:288 M:283 W: Missing Blank Line separator, <400> field identifier  
L:496 M:283 W: Missing Blank Line separator, <220> field identifier  
L:496 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:508 M:283 W: Missing Blank Line separator, <220> field identifier  
L:509 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:511 M:283 W: Missing Blank Line separator, <400> field identifier  
L:518 M:283 W: Missing Blank Line separator, <220> field identifier  
L:519 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:521 M:283 W: Missing Blank Line separator, <400> field identifier  
L:528 M:283 W: Missing Blank Line separator, <220> field identifier  
L:529 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:531 M:283 W: Missing Blank Line separator, <400> field identifier  
L:539 M:283 W: Missing Blank Line separator, <220> field identifier  
L:540 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:552 M:283 W: Missing Blank Line separator, <220> field identifier  
L:553 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:555 M:283 W: Missing Blank Line separator, <400> field identifier  
L:562 M:283 W: Missing Blank Line separator, <220> field identifier  
L:563 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:565 M:283 W: Missing Blank Line separator, <400> field identifier  
L:572 M:283 W: Missing Blank Line separator, <220> field identifier  
L:573 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:575 M:283 W: Missing Blank Line separator, <400> field identifier  
L:582 M:283 W: Missing Blank Line separator, <220> field identifier  
L:583 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:585 M:283 W: Missing Blank Line separator, <400> field identifier  
L:592 M:283 W: Missing Blank Line separator, <220> field identifier  
L:593 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
L:595 M:283 W: Missing Blank Line separator, <400> field identifier  
L:602 M:283 W: Missing Blank Line separator, <220> field identifier  
L:603 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:605 M:283 W: Missing Blank Line separator, <400> field identifier  
L:612 M:283 W: Missing Blank Line separator, <220> field identifier  
L:613 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:615 M:283 W: Missing Blank Line separator, <400> field identifier  
L:622 M:283 W: Missing Blank Line separator, <220> field identifier  
L:623 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:625 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
TIME: 07:15:10

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

L:632 M:283 W: Missing Blank Line separator, <220> field identifier  
L:632 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:635 M:283 W: Missing Blank Line separator, <400> field identifier  
L:643 M:283 W: Missing Blank Line separator, <220> field identifier  
L:643 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:646 M:283 W: Missing Blank Line separator, <400> field identifier  
L:654 M:283 W: Missing Blank Line separator, <220> field identifier  
L:654 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:657 M:283 W: Missing Blank Line separator, <400> field identifier  
L:665 M:283 W: Missing Blank Line separator, <220> field identifier  
L:668 M:283 W: Missing Blank Line separator, <300> field identifier  
L:669 M:283 W: Missing Blank Line separator, <400> field identifier  
L:676 M:254 E: (42) Number of Bases conflicts Running Total, LENGTH:Input:114 Counted:144  
L:946 M:283 W: Missing Blank Line separator, <220> field identifier  
L:947 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:949 M:283 W: Missing Blank Line separator, <400> field identifier  
L:956 M:283 W: Missing Blank Line separator, <220> field identifier  
L:957 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21  
L:959 M:283 W: Missing Blank Line separator, <400> field identifier  
L:967 M:283 W: Missing Blank Line separator, <220> field identifier  
L:968 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22  
L:970 M:283 W: Missing Blank Line separator, <400> field identifier  
L:977 M:283 W: Missing Blank Line separator, <220> field identifier  
L:978 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23  
L:980 M:283 W: Missing Blank Line separator, <400> field identifier  
L:987 M:283 W: Missing Blank Line separator, <220> field identifier  
L:987 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:999 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1010 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1021 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1032 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1043 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1054 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1066 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1312 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:1179 Counted:1218  
L:1504 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:943 Counted:963  
L:1769 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:1338 Counted:1367